

Sequence Listing

(1) GENERAL INFORMATION:

(i) APPLICANT::

- (A) NAME: Max-Planck-Gesellschaft zur Förderung der
Wissenschaften e.V.
- (B) STREET:: none
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) ZIP CODE: none

(ii) TITLE OF THE INVENTION: Nucleic acid molecules encoding proteins
which impart the adhesion of Neisseria cells to human cells

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(vi) DATA OF PRIOR APPLICATION:

- (A) APPLICATION NUMBER: DE 19534579.7
- (B) FILING DATE: 18-SEP-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3287 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

- (A) ORGANISM: Neisseria gonorrhoeae
- (B) STRAIN: MS11

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: genomic library in pBA
- (B) CLONE(S): H1967/pES25

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 136..447

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:583..1542

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1585..3111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGCGCAAAC GCGGACGCT GCTGTTAGCC CCGCTTGAAA CAAATGCCGT CTGAACGCCA	60
CTTCAGACGG CATTTTATA ATAAGGCGCT GTCCTAGATA ACTAGGGAAA TTCAAATTAA	120
GTTAGAATTA TCCCT ATG AGA AAA AGC CGT CTA AGC CGG TAT AAA CAA AAT	171
Met Arg Lys Ser Arg Leu Ser Arg Tyr Lys Gln Asn	
1 5 10	
AAA CTC ATT GAA CTG TTT GTC GCA GGC GTA ACT GCA AGA ACA GCA GCA	219
Lys Leu Ile Glu Leu Phe Val Ala Gly Val Thr Ala Arg Thr Ala Ala	
15 20 25	
GAG CCT GAC AGC ATT GTT TAT ACG GAT TGT TAT CGT CGC TAT GAT GTA	267
Glu Pro Asp Ser Ile Val Tyr Thr Asp Cys Tyr Arg Arg Tyr Asp Val	
30 35 40	
TTG GAT GCG GGC GAA TTT AGC CAT TTC CGT ATC AAT CAC AGC ACA CAT	315
Leu Asp Ala Gly Glu Phe Ser His Phe Arg Ile Asn His Ser Thr His	
45 50 55 60	
TTT GCC GAA CGA CAA AAC CAT ATT AAT GGA ATT GGG AAC TTT TGG AAC	363
Phe Ala Glu Arg Gln Asn His Ile Asn Gly Ile Gly Asn Phe Trp Asn	
65 70 75	
CGG GCA AAA CGT CAT TTA CGC AAG TTT GAC GGC ATT CCC AAA GAG CAT	411
Arg Ala Lys Arg His Leu Arg Lys Phe Asp Gly Ile Pro Lys Glu His	
80 85 90	
TTT GAG CCG TAT TTA AAG GAG TGC GAA CGG CGT TTT TAACAACAGT	457
Phe Glu Pro Tyr Leu Lys Glu Cys Glu Arg Arg Phe	
95 100	
GAGATAAAAG TTCTTGTTCC ATTTTAAAC AATTAGTAAA ATCGAGTTTA TCCTAGTTGT	517
CCAGGACGGC CCCTAATTTA TTTACAATTT TGATACAATT TGTTTTTCAT CAAAGGAGAA	577
AATCT ATG CGG GCA CGG CTG CTG ATA CCT ATT CTT TTT TCG GTT TTT	624
Met Arg Ala Arg Leu Leu Ile Pro Ile Leu Phe Ser Val Phe	
1 5 10	
ATT TTA TCC GCC TGC GGG ACA CTG ACA GGT ATT CCA TCG CAT GGC GGA	672
Ile Leu Ser Ala Cys Gly Thr Leu Thr Gly Ile Pro Ser His Gly Gly	
15 20 25 30	

GGC AAA CGC TTC GCG GTC GAA CAA GAA CTT GTG GCC GCT TCT GCC AGA	720
Gly Lys Arg Phe Ala Val Glu Gln Glu Leu Val Ala Ala Ser Ala Arg	
35 40 45	
GCT GCC GTT AAA GAC ATG GAT TTA CAG GCA TTA CAC GGA CGA AAA GTT	768
Ala Ala Val Lys Asp Met Asp Leu Gln Ala Leu His Gly Arg Lys Val	
50 55 60	
GCA TTG TAC ATT GCA ACT ATG GGC GAC CAA GGT TCA GGC AGT TTG ACA	816
Ala Leu Tyr Ile Ala Thr Met Gly Asp Gln Gly Ser Gly Ser Leu Thr	
65 70 75	
GGG GGT CGC TAC TCC ATT GAT GCA CTG ATT CGC GGC GAA TAC ATA AAC	864
Gly Gly Arg Tyr Ser Ile Asp Ala Leu Ile Arg Gly Glu Tyr Ile Asn	
80 85 90	
AGC CCT GCC GTC CGC ACC GAT TAC ACC TAT CCG CGT TAC GAA ACC ACC	912
Ser Pro Ala Val Arg Thr Asp Tyr Thr Tyr Pro Arg Tyr Glu Thr Thr	
95 100 105 110	
GCT GAA ACA ACA TCA GGC GGT TTG ACG GGT TTA ACC ACT TCT TTA TCT	960
Ala Glu Thr Thr Ser Gly Gly Leu Thr Gly Leu Thr Thr Ser Leu Ser	
115 120 125	
ACA CTT AAT GCC CCT GCA CTC TCG CGC ACC CAA TCA GAC GGT AGC GGA	1008
Thr Leu Asn Ala Pro Ala Leu Ser Arg Thr Gln Ser Asp Gly Ser Gly	
130 135 140	
AGT AGG AGC AGT CTG GGC TTA AAT ATT GGC GGG ATG GGG GAT TAT CGA	1056
Ser Arg Ser Ser Leu Gly Leu Asn Ile Gly Gly Met Gly Asp Tyr Arg	
145 150 155	
AAT GAA ACC TTG ACG ACC AAC CCG CGC GAC ACT GCC TTT CTT TCC CAC	1104
Asn Glu Thr Leu Thr Thr Asn Pro Arg Asp Thr Ala Phe Leu Ser His	
160 165 170	
TTG GTA CAG ACC GTA TTT TTC CTG CGC GGC ATA GAC GTT GTT TCT CCT	1152
Leu Val Gln Thr Val Phe Phe Leu Arg Gly Ile Asp Val Val Ser Pro	
175 180 185 190	
GCC AAT GCC GAT ACA GAT GTG TTT ATT AAC ATC GAC GTA TTC GGA ACG	1200
Ala Asn Ala Asp Thr Asp Val Phe Ile Asn Ile Asp Val Phe Gly Thr	
195 200 205	
ATA CGC AAC AGA ACC GAA ATG CAC CTA TAC AAT GCC GAA ACA CTG AAA	1248
Ile Arg Asn Arg Thr Glu Met His Leu Tyr Asn Ala Glu Thr Leu Lys	
210 215 220	
GCC CAA ACA AAA CTG GAA TAT TTC GCA GTA GAC AGA ACC AAT AAA AAA	1296
Ala Gln Thr Lys Leu Glu Tyr Phe Ala Val Asp Arg Thr Asn Lys Lys	
225 230 235	
TTG CTC ATC AAA CCC AAA ACC AAT GCG TTT GAA GCT GCC TAT AAA GAA	1344
Leu Leu Ile Lys Pro Lys Thr Asn Ala Phe Glu Ala Ala Tyr Lys Glu	
240 245 250	

AAT TAC GCA TTG TGG ATG GGG CCG TAT AAA GTA AGC AAA GGA ATC AAA Asn Tyr Ala Leu Trp Met Gly Pro Tyr Lys Val Ser Lys Gly Ile Lys 255 260 265 270	1392
CCG ACG GAA GGA TTA ATG GTC GAT TTC TCC GAT ATC CGG CCA TAC GGC Pro Thr Glu Gly Leu Met Val Asp Phe Ser Asp Ile Arg Pro Tyr Gly 275 280 285	1440
AAT CAT ACG GGT AAC TCC GCC CCA TCC GTA GAG GCT GAT AAC AGT CAT Asn His Thr Gly Asn Ser Ala Pro Ser Val Glu Ala Asp Asn Ser His 290 295 300	1488
GAG GGG TAT GGA TAC AGC GAT GAA GCA GTG CGA CAA CAT AGA CAA GGG Glu Gly Tyr Gly Tyr Ser Asp Glu Ala Val Arg Gln His Arg Gln Gly 305 310 315	1536
CAA CCT TGATTACAC TGCCATAACC GCTTGCTGCC AAGGAAAACA AA ATG AAT Gln Pro Met Asn 320 1	1590
TTG CCT ATT CAA AAA TTC ATG ATG CTG TTT GCA GCG GCA ATA TCG TTG Leu Pro Ile Gln Lys Phe Met Met Leu Phe Ala Ala Ala Ile Ser Leu 5 10 15	1638
CTG CAA ATC CCC ATT AGT CAT GCG AAC GGT TTG GAT GCC CGT TTG CGC Leu Gln Ile Pro Ile Ser His Ala Asn Gly Leu Asp Ala Arg Leu Arg 20 25 30	1686
GAT GAT ATG CAG GCA AAA CAC TAC GAA CCG GGT GGC AAA TAC CAT CTG Asp Asp Met Gln Ala Lys His Tyr Glu Pro Gly Gly Lys Tyr His Leu 35 40 45 50	1734
TTC GGT AAT GCT CGC GGC AGT GTT AAA AAT CGG GTT TGC GCC GTC CAA Phe Gly Asn Ala Arg Gly Ser Val Lys Asn Arg Val Cys Ala Val Gln 55 60 65	1782
ACA TTT GAT GCA ACT GCG GTC GGC CCC ATA CTG CCT ATT ACA CAC GAA Thr Phe Asp Ala Thr Ala Val Gly Pro Ile Leu Pro Ile Thr His Glu 70 75 80	1830
CGG ACA GGG TTT GAA GGC ATT ATC GGT TAT GAA ACC CAT TTT TCA GGA Arg Thr Gly Phe Glu Gly Ile Ile Gly Tyr Glu Thr His Phe Ser Gly 85 90 95	1878
CAC GGA CAC GAA GTA CAC AGT CCG TTC GAT AAT CAT GAT TCA AAA AGC His Gly His Glu Val His Ser Pro Phe Asp Asn His Asp Ser Lys Ser 100 105 110	1926
ACT TCT GAT TTC AGC GGC GGC GTA GAC GGC GGT TTT ACC GTT TAC CAA Thr Ser Asp Phe Ser Gly Gly Val Asp Gly Gly Phe Thr Val Tyr Gln 115 120 125 130	1974
CTT CAT CGG ACA GGG TCG GAA ATA CAT CCC GCA GAC GGA TAT GAC GGG Leu His Arg Thr Gly Ser Glu Ile His Pro Ala Asp Gly Tyr Asp Gly 135 140 145	2022

CCT CAA GGC GGC GGT TAT CCG GAA CCA CAA GGG GCA AGG GAT ATA TAC	2070
Pro Gln Gly Gly Gly Tyr Pro Glu Pro Gln Gly Ala Arg Asp Ile Tyr	
150 155 160	
AGC TAC CAT ATC AAA GGA ACT TCA ACC AAA ACA AAG ATA AAC ACT GTT	2118
Ser Tyr His Ile Lys Gly Thr Ser Thr Lys Thr Lys Ile Asn Thr Val	
165 170 175	
CCG CAA GCC CCT TTT TCA GAC CGC TGG CTA AAA GAA AAT GCC GGT GCC	2166
Pro Gln Ala Pro Phe Ser Asp Arg Trp Leu Lys Glu Asn Ala Gly Ala	
180 185 190	
GCT TCC GGT TTT CTC AGC CGT GCG GAT GAA GCA GGA AAA CTG ATA TGG	2214
Ala Ser Gly Phe Leu Ser Arg Ala Asp Glu Ala Gly Lys Leu Ile Trp	
195 200 205 210	
GAA AAC GAC CCC GAT AAA AAT TGG CGG GCT AAC CGT ATG GAT GAT ATT	2262
Glu Asn Asp Pro Asp Lys Asn Trp Arg Ala Asn Arg Met Asp Asp Ile	
215 220 225	
CGC GGC ATC GTC CAA GGT GCG GTT AAT CCT TTT TTA ACG GGT TTT CAG	2310
Arg Gly Ile Val Gln Gly Ala Val Asn Pro Phe Leu Thr Gly Phe Gln	
230 235 240	
GGA TTG GGA GTT GGG GCA ATT ACA GAC AGT GCG GTA AGC CCG GTA ACC	2358
Gly Leu Gly Val Gly Ala Ile Thr Asp Ser Ala Val Ser Pro Val Thr	
245 250 255	
TAT GCG GCA GCA CGG AAA ACT TTA CAG GGT ATT CAC AAT TTA GGA AAT	2406
Tyr Ala Ala Ala Arg Lys Thr Leu Gln Gly Ile His Asn Leu Gly Asn	
260 265 270	
TTA AGT CCG GAA GCA CAA CTT GCC GCC GCG AGC CTA TTA CAG GAC AGT	2454
Leu Ser Pro Glu Ala Gln Leu Ala Ala Ala Ser Leu Leu Gln Asp Ser	
275 280 285 290	
GCC TTT GCG GTA AAA GAC GGC ATC AAT TCC GCC AGA CAA TGG GCT GAT	2502
Ala Phe Ala Val Lys Asp Gly Ile Asn Ser Ala Arg Gln Trp Ala Asp	
295 300 305	
GCC CAT CCG AAT ATA ACA GCA ACA GCC CAA ACT GCC CTT GCC GTA GCA	2550
Ala His Pro Asn Ile Thr Ala Thr Ala Gln Thr Ala Leu Ala Val Ala	
310 315 320	
GAG GCT GCA GGT ACG GTT TGG GGA GGT AAA AAA GTA GAA CTT AAC CCG	2598
Glu Ala Ala Gly Thr Val Trp Gly Gly Lys Lys Val Glu Leu Asn Pro	
325 330 335	
ACC AAA TGG GAT TGG GTT AAA AAT ACC GGC TAT GAA AAA CCT GCT GCC	2646
Thr Lys Trp Asp Trp Val Lys Asn Thr Gly Tyr Glu Lys Pro Ala Ala	
340 345 350	
CGA CCT ATG CAG ACT GTA GAC GGG GAA ATG GCC GGG AAA AAT AAG CCA	2694
Arg Pro Met Gln Thr Val Asp Gly Glu Met Ala Gly Lys Asn Lys Pro	
355 360 365 370	

CCG AAA CCA AGT ACG CAG CAA CAC TCT ACA CAC TCT GAT AAC AAT ATC	2742
Pro Lys Pro Ser Thr Gln Gln His Ser Thr His Ser Asp Asn Asn Ile	
375 380 385	
GGC TTA CCT GCC CCA TAT GTT AAA CCT GAT ACA TCT ATT TCT CCG ACA	2790
Gly Leu Pro Ala Pro Tyr Val Lys Pro Asp Thr Ser Ile Ser Pro Thr	
390 395 400	
GGA ACA ATT CAA GAC CGC ATC AGA TGG ACA AAA TCC AAG TTT CCT ACT	2838
Gly Thr Ile Gln Asp Arg Ile Arg Trp Thr Lys Ser Lys Phe Pro Thr	
405 410 415	
GAG AAA TCT TTA AAT GGA CAT TTC AAA GCT CAT GGA AAA GAA TTT GGC	2886
Glu Lys Ser Leu Asn Gly His Phe Lys Ala His Gly Lys Glu Phe Gly	
420 425 430	
GAT ATA ACC ATT GAA GAC TAC CAA AAA ATG GCG TCT GAT TTG TTA TCA	2934
Asp Ile Thr Ile Glu Asp Tyr Gln Lys Met Ala Ser Asp Leu Leu Ser	
435 440 445 450	
AAA CAG ACA TCG GAC AAG ATA TTA GGT TAT CAG ACG GAA CAT AGA CGA	2982
Lys Gln Thr Ser Asp Lys Ile Leu Gly Tyr Gln Thr Glu His Arg Arg	
455 460 465	
GTG CGC TAT GAT ATC AAT AAC AAT ATC TAT GTT TTG GCC AAT CCA AAA	3030
Val Arg Tyr Asp Ile Asn Asn Asn Ile Tyr Val Leu Ala Asn Pro Lys	
470 475 480	
ACA TTC AAA ATC AAA ACA ATG TTT AAA CCA AAC TTA GGA AAG GAG TAT	3078
Thr Phe Lys Ile Lys Thr Met Phe Lys Pro Asn Leu Gly Lys Glu Tyr	
485 490 495	
TAT GAT GGA GAA TTC AAA AAA GAC ATG GGA AAT TGACGGAGAA ATATGGCTAC	3131
Tyr Asp Gly Glu Phe Lys Lys Asp Met Gly Asn	
500 505	
ATTGTCCTGT TTGCGGAACCT GAAGTTATGG ACTATGATAT CTGTGACGTT TGTCAGTGGC	3191
AAAATACAGG AGAAACTAAT ATAGATGGTG GTCCTAATGA AATGACACTT GCGGAGGCGA	3251
AAGAAGCTTA CGCAAAAGGC TTACCAATCA GATAAA	3287

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1136 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*

(B) STRAIN: MS11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:135..1094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AACAACAGTG AGATAAAAGT TCTTGTTCCA TTTTAAACA ATTAGTAAAA TCGAGTTTAT	60
CCTAGTTGTC CAGGACGGCC CCTAATTTAT TTACAATTTT GATACAATTT GTTTTTCATC	120
AAAGGAGAAA ATCT ATG CGG GCA CGG CTG CTG ATA CCT ATT CTT TTT TCG	170
Met Arg Ala Arg Leu Leu Ile Pro Ile Leu Phe Ser	
510 515 520	
GTT TTT ATT TTA TCC GCC TGC GGG ACA CTG ACA GGT ATT CCA TCG CAT	218
Val Phe Ile Leu Ser Ala Cys Gly Thr Leu Thr Gly Ile Pro Ser His	
525 530 535	
GGC GGA GGC AAA CGC TTC GCG GTC GAA CAA GAA CTT GTG GCC GCT TCT	266
Gly Gly Gly Lys Arg Phe Ala Val Glu Gln Glu Leu Val Ala Ala Ser	
540 545 550	
GCC AGA GCT GCC GTT AAA GAC ATG GAT TTA CAG GCA TTA CAC GGA CGA	314
Ala Arg Ala Ala Val Lys Asp Met Asp Leu Gln Ala Leu His Gly Arg	
555 560 565	
AAA GTT GCA TTG TAC ATT GCA ACT ATG GGC GAC CAA GGT TCA GGC AGT	362
Lys Val Ala Leu Tyr Ile Ala Thr Met Gly Asp Gln Gly Ser Gly Ser	
570 575 580 585	
TTG ACA GGG GGT CGC TAC TCC ATT GAT GCA CTG ATT CGC GGC GAA TAC	410
Leu Thr Gly Gly Arg Tyr Ser Ile Asp Ala Leu Ile Arg Gly Glu Tyr	
590 595 600	
ATA AAC AGC CCT GCC GTC CGC ACC GAT TAC ACC TAT CCG CGT TAC GAA	458
Ile Asn Ser Pro Ala Val Arg Thr Asp Tyr Thr Tyr Pro Arg Tyr Glu	
605 610 615	
ACC ACC GCT GAA ACA ACA TCA GGC GGT TTG ACG GGT TTA ACC ACT TCT	506
Thr Thr Ala Glu Thr Thr Ser Gly Gly Leu Thr Gly Leu Thr Thr Ser	
620 625 630	
TTA TCT ACA CTT AAT GCC CCT GCA CTC TCG CGC ACC CAA TCA GAC GGT	554
Leu Ser Thr Leu Asn Ala Pro Ala Leu Ser Arg Thr Gln Ser Asp Gly	
635 640 645	
AGC GGA AGT AGG AGC AGT CTG GGC TTA AAT ATT GGC GGG ATG GGG GAT	602
Ser Gly Ser Arg Ser Ser Leu Gly Leu Asn Ile Gly Gly Met Gly Asp	
650 655 660 665	

TAT CGA AAT GAA ACC TTG ACG ACC AAC CCG CGC GAC ACT GCC TTT CTT Tyr Arg Asn Glu Thr Leu Thr Thr Asn Pro Arg Asp Thr Ala Phe Leu 670 675 680	650
TCC CAC TTG GTA CAG ACC GTA TTT TTC CTG CGC GGC ATA GAC GTT GTT Ser His Leu Val Gln Thr Val Phe Phe Leu Arg Gly Ile Asp Val Val 685 690 695	698
TCT CCT GCC AAT GCC GAT ACA GAT GTG TTT ATT AAC ATC GAC GTA TTC Ser Pro Ala Asn Ala Asp Thr Asp Val Phe Ile Asn Ile Asp Val Phe 700 705 710	746
GGA ACG ATA CGC AAC AGA ACC GAA ATG CAC CTA TAC AAT GCC GAA ACA Gly Thr Ile Arg Asn Arg Thr Glu Met His Leu Tyr Asn Ala Glu Thr 715 720 725	794
CTG AAA GCC CAA ACA AAA CTG GAA TAT TTC GCA GTA GAC AGA ACC AAT Leu Lys Ala Gln Thr Lys Leu Glu Tyr Phe Ala Val Asp Arg Thr Asn 730 735 740 745	842
AAA AAA TTG CTC ATC AAA CCC AAA ACC AAT GCG TTT GAA GCT GCC TAT Lys Lys Leu Leu Ile Lys Pro Lys Thr Asn Ala Phe Glu Ala Ala Tyr 750 755 760	890
AAA GAA AAT TAC GCA TTG TGG ATG GGG CCG TAT AAA GTA AGC AAA GGA Lys Glu Asn Tyr Ala Leu Trp Met Gly Pro Tyr Lys Val Ser Lys Gly 765 770 775	938
ATC AAA CCG ACG GAA GGA TTA ATG GTC GAT TTC TCC GAT ATC CGG CCA Ile Lys Pro Thr Glu Gly Leu Met Val Asp Phe Ser Asp Ile Arg Pro 780 785 790	986
TAC GGC AAT CAT ACG GGT AAC TCC GCC CCA TCC GTA GAG GCT GAT AAC Tyr Gly Asn His Thr Gly Asn Ser Ala Pro Ser Val Glu Ala Asp Asn 795 800 805	1034
AGT CAT GAG GGG TAT GGA TAC AGC GAT GAA GCA GTG CGA CAA CAT AGA Ser His Glu Gly Tyr Gly Tyr Ser Asp Glu Ala Val Arg Gln His Arg 810 815 820 825	1082
CAA GGG CAA CCT TGATTACAC TGCCATAACC GCTTGCTGCC AAGGAAAACA Gln Gly Gln Pro	1134
AA	1136

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(B) STRAIN: MS11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:136..447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

CGGCGCAAAC GGCGGACGCT GCTGTTAGCC CCGCTTGAAA CAAATGCCGT CTGAACGCCA      60
CTTCAGACGG CATTTTATA ATAAGGCGCT GTCCTAGATA ACTAGGGAAA TTCAAATTAA      120
GTTAGAATTA TCCCT ATG AGA AAA AGC CGT CTA AGC CGG TAT AAA CAA AAT      171
               Met Arg Lys Ser Arg Leu Ser Arg Tyr Lys Gln Asn
                   325                               330

AAA CTC ATT GAA CTG TTT GTC GCA GGC GTA ACT GCA AGA ACA GCA GCA      219
Lys Leu Ile Glu Leu Phe Val Ala Gly Val Thr Ala Arg Thr Ala Ala
               335                               340                               345

GAG CCT GAC AGC ATT GTT TAT ACG GAT TGT TAT CGT CGC TAT GAT GTA      267
Glu Pro Asp Ser Ile Val Tyr Thr Asp Cys Tyr Arg Arg Tyr Asp Val
               350                               355                               360

TTG GAT GCG GGC GAA TTT AGC CAT TTC CGT ATC AAT CAC AGC ACA CAT      315
Leu Asp Ala Gly Glu Phe Ser His Phe Arg Ile Asn His Ser Thr His
               365                               370                               375                               380

TTT GCC GAA CGA CAA AAC CAT ATT AAT GGA ATT GGG AAC TTT TGG AAC      363
Phe Ala Glu Arg Gln Asn His Ile Asn Gly Ile Gly Asn Phe Trp Asn
                   385                               390                               395

CGG GCA AAA CGT CAT TTA CGC AAG TTT GAC GGC ATT CCC AAA GAG CAT      411
Arg Ala Lys Arg His Leu Arg Lys Phe Asp Gly Ile Pro Lys Glu His
                   400                               405                               410

TTT GAG CCG TAT TTA AAG GAG TGC GAA CGG CGT TTT TAACAACAGT      457
Phe Glu Pro Tyr Leu Lys Glu Cys Glu Arg Arg Phe
               415                               420

GAGATAAAAG TTCTGTTCC ATTTTAAAC AATTAGTAAA ATCGAGTTTA TCCTAGTTGT      517
CCAGGACGGC CCCTAATTTA TTTACAATTT TGATACAATT TGTTTTTCAT CAAAGGAGAA      577
AATCT                                                                 582

```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1744 base pairs

(B) TYPE: Nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: MS11

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 42..1568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATTCACACT GCCATAACCG CTTGCTGCCA AGGAAAACAA A ATG AAT TTG CCT	53
Met Asn Leu Pro	
105	
ATT CAA AAA TTC ATG ATG CTG TTT GCA GCG GCA ATA TCG TTG CTG CAA	101
Ile Gln Lys Phe Met Met Leu Phe Ala Ala Ala Ile Ser Leu Leu Gln	
110 115 120	
ATC CCC ATT AGT CAT GCG AAC GGT TTG GAT GCC CGT TTG CGC GAT GAT	149
Ile Pro Ile Ser His Ala Asn Gly Leu Asp Ala Arg Leu Arg Asp Asp	
125 130 135 140	
ATG CAG GCA AAA CAC TAC GAA CCG GGT GGC AAA TAC CAT CTG TTC GGT	197
Met Gln Ala Lys His Tyr Glu Pro Gly Gly Lys Tyr His Leu Phe Gly	
145 150 155	
AAT GCT CGC GGC AGT GTT AAA AAT CGG GTT TGC GCC GTC CAA ACA TTT	245
Asn Ala Arg Gly Ser Val Lys Asn Arg Val Cys Ala Val Gln Thr Phe	
160 165 170	
GAT GCA ACT GCG GTC GGC CCC ATA CTG CCT ATT ACA CAC GAA CGG ACA	293
Asp Ala Thr Ala Val Gly Pro Ile Leu Pro Ile Thr His Glu Arg Thr	
175 180 185	
GGG TTT GAA GGC ATT ATC GGT TAT GAA ACC CAT TTT TCA GGA CAC GGA	341
Gly Phe Glu Gly Ile Ile Gly Tyr Glu Thr His Phe Ser Gly His Gly	
190 195 200	
CAC GAA GTA CAC AGT CCG TTC GAT AAT CAT GAT TCA AAA AGC ACT TCT	389
His Glu Val His Ser Pro Phe Asp Asn His Asp Ser Lys Ser Thr Ser	
205 210 215 220	
GAT TTC AGC GGC GGC GTA GAC GGC GGT TTT ACC GTT TAC CAA CTT CAT	437
Asp Phe Ser Gly Gly Val Asp Gly Gly Phe Thr Val Tyr Gln Leu His	
225 230 235	
CGG ACA GGG TCG GAA ATA CAT CCC GCA GAC GGA TAT GAC GGG CCT CAA	485
Arg Thr Gly Ser Glu Ile His Pro Ala Asp Gly Tyr Asp Gly Pro Gln	

240	245	250	
GGC GGC GGT TAT CCG GAA CCA CAA GGG GCA AGG GAT ATA TAC AGC TAC Gly Gly Gly Tyr Pro Glu Pro Gln Gly Ala Arg Asp Ile Tyr Ser Tyr 255 260 265			533
CAT ATC AAA GGA ACT TCA ACC AAA ACA AAG ATA AAC ACT GTT CCG CAA His Ile Lys Gly Thr Ser Thr Lys Thr Lys Ile Asn Thr Val Pro Gln 270 275 280			581
GCC CCT TTT TCA GAC CGC TGG CTA AAA GAA AAT GCC GGT GCC GCT TCC Ala Pro Phe Ser Asp Arg Trp Leu Lys Glu Asn Ala Gly Ala Ala Ser 285 290 295 300			629
GGT TTT CTC AGC CGT GCG GAT GAA GCA GGA AAA CTG ATA TGG GAA AAC Gly Phe Leu Ser Arg Ala Asp Glu Ala Gly Lys Leu Ile Trp Glu Asn 305 310 315			677
GAC CCC GAT AAA AAT TGG CGG GCT AAC CGT ATG GAT GAT ATT CGC GGC Asp Pro Asp Lys Asn Trp Arg Ala Asn Arg Met Asp Asp Ile Arg Gly 320 325 330			725
ATC GTC CAA GGT GCG GTT AAT CCT TTT TTA ACG GGT TTT CAG GGA TTG Ile Val Gln Gly Ala Val Asn Pro Phe Leu Thr Gly Phe Gln Gly Leu 335 340 345			773
GGA GTT GGG GCA ATT ACA GAC AGT GCG GTA AGC CCG GTA ACC TAT GCG Gly Val Gly Ala Ile Thr Asp Ser Ala Val Ser Pro Val Thr Tyr Ala 350 355 360			821
GCA GCA CGG AAA ACT TTA CAG GGT ATT CAC AAT TTA GGA AAT TTA AGT Ala Ala Arg Lys Thr Leu Gln Gly Ile His Asn Leu Gly Asn Leu Ser 365 370 375 380			869
CCG GAA GCA CAA CTT GCC GCC GCG AGC CTA TTA CAG GAC AGT GCC TTT Pro Glu Ala Gln Leu Ala Ala Ala Ser Leu Leu Gln Asp Ser Ala Phe 385 390 395			917
GCG GTA AAA GAC GGC ATC AAT TCC GCC AGA CAA TGG GCT GAT GCC CAT Ala Val Lys Asp Gly Ile Asn Ser Ala Arg Gln Trp Ala Asp Ala His 400 405 410			965
CCG AAT ATA ACA GCA ACA GCC CAA ACT GCC CTT GCC GTA GCA GAG GCT Pro Asn Ile Thr Ala Thr Ala Gln Thr Ala Leu Ala Val Ala Glu Ala 415 420 425			1013
GCA GGT ACG GTT TGG GGA GGT AAA AAA GTA GAA CTT AAC CCG ACC AAA Ala Gly Thr Val Trp Gly Gly Lys Lys Val Glu Leu Asn Pro Thr Lys 430 435 440			1061

TGG GAT TGG GTT AAA AAT ACC GGC TAT GAA AAA CCT GCT GCC CGA CCT	1109
Trp Asp Trp Val Lys Asn Thr Gly Tyr Glu Lys Pro Ala Ala Arg Pro	
445 450 455 460	
ATG CAG ACT GTA GAC GGG GAA ATG GCC GGG AAA AAT AAG CCA CCG AAA	1157
Met Gln Thr Val Asp Gly Glu Met Ala Gly Lys Asn Lys Pro Pro Lys	
465 470 475	
CCA AGT ACG CAG CAA CAC TCT ACA CAC TCT GAT AAC AAT ATC GGC TTA	1205
Pro Ser Thr Gln Gln His Ser Thr His Ser Asp Asn Asn Ile Gly Leu	
480 485 490	
CCT GCC CCA TAT GTT AAA CCT GAT ACA TCT ATT TCT CCG ACA GGA ACA	1253
Pro Ala Pro Tyr Val Lys Pro Asp Thr Ser Ile Ser Pro Thr Gly Thr	
495 500 505	
ATT CAA GAC CGC ATC AGA TGG ACA AAA TCC AAG TTT CCT ACT GAG AAA	1301
Ile Gln Asp Arg Ile Arg Trp Thr Lys Ser Lys Phe Pro Thr Glu Lys	
510 515 520	
TCT TTA AAT GGA CAT TTC AAA GCT CAT GGA AAA GAA TTT GGC GAT ATA	1349
Ser Leu Asn Gly His Phe Lys Ala His Gly Lys Glu Phe Gly Asp Ile	
525 530 535 540	
ACC ATT GAA GAC TAC CAA AAA ATG GCG TCT GAT TTG TTA TCA AAA CAG	1397
Thr Ile Glu Asp Tyr Gln Lys Met Ala Ser Asp Leu Leu Ser Lys Gln	
545 550 555	
ACA TCG GAC AAG ATA TTA GGT TAT CAG ACG GAA CAT AGA CGA GTG CGC	1445
Thr Ser Asp Lys Ile Leu Gly Tyr Gln Thr Glu His Arg Arg Val Arg	
560 565 570	
TAT GAT ATC AAT AAC AAT ATC TAT GTT TTG GCC AAT CCA AAA ACA TTC	1493
Tyr Asp Ile Asn Asn Asn Ile Tyr Val Leu Ala Asn Pro Lys Thr Phe	
575 580 585	
AAA ATC AAA ACA ATG TTT AAA CCA AAC TTA GGA AAG GAG TAT TAT GAT	1541
Lys Ile Lys Thr Met Phe Lys Pro Asn Leu Gly Lys Glu Tyr Tyr Asp	
590 595 600	
GGA GAA TTC AAA AAA GAC ATG GGA AAT TGACGGAGAA ATATGGCTAC	1588
Gly Glu Phe Lys Lys Asp Met Gly Asn	
605 610	
ATTGTCCTGT TTGCGGAAC TGAAGTTATGG ACTATGATAT CTGTGACGTT TGTCAGTGGC	1648
AAAATACAGG AGAACTAAT ATAGATGGTG GTCCTAATGA AATGACACTT GCGGAGGCGA	1708
AAGAAGCTTA CGCAAAGGC TTACCAATCA GATAAA	1744